Figure 1:

1/1

```
GGT ACC ACT TCT CTC AAT CCA ACT TTC TAA ACA ATG GCT TCT AAA CCT TTC TTG TCT CTT
                                                M   A   S   K   P   F   L   S   L
```

61/10

```
CTT TCT TTG TCT TTG CTT TTG TTC ACC TCT ACT AGT TTG GCT GAC CTG TAC TTC ATT TTG
L   S   L   S   L   L   L   F   T   S   T   S   L   A   D   L   Y   F   I   L
```

121/30

```
GAC AAA TCA GGA AGT GTG CTG CAC CAC TGG AAT GAA ATC TAT TAC TTT GTG GAA CAG TTG
D   K   S   G   S   V   L   H   H   W   N   E   I   Y   Y   F   V   E   Q   L
```

181/50

```
GCT CAC AAA TTC ATC AGC CCA CAG TTG AGA ATG TCC TTT ATT GTT TTC TCC ACC CGA GGA
A   H   K   F   I   S   P   Q   L   R   M   S   F   I   V   F   S   T   R   G
```

241/70

```
ACA ACC TTA ATG AAA CTG ACA GAA GAC AGA GAA CAA ATC CGT CAA GGC CTA GAA GAA CTC
T   T   L   M   K   L   T   E   D   R   E   Q   I   R   Q   G   L   E   E   L
```

301/90

```
CAG AAA GTT CTG CCA GGA GGA GAC ACT TAC ATG CAT GAA GGA TTT GAA AGG GCC AGT GAG
Q   K   V   L   P   G   G   D   T   Y   M   H   E   G   F   E   R   A   S   E
```

361/110

```
CAG ATT TAT TAT GAA AAC AGA CAA GGG TAC AGG ACA GCC AGC GTC ATC ATT GCT TTG ACT
Q   I   Y   Y   E   N   R   Q   G   Y   R   T   A   S   V   I   I   A   L   T
```

421/130

```
GAT GGA GAA CTC CAT GAA GAT CTC TTT TTC TAT TCA GAG AGG GAG GCT AAT AGG TCT CGA
D   G   E   L   H   E   D   L   F   F   Y   S   E   R   E   A   N   R   S   R
```

481/150

```
GAT CTT GGT GCA ATT GTT TAC TGT GTT GGT GTG AAA GAT TTC AAT GAG ACA CAG CTG GCC
D   L   G   A   I   V   Y   C   V   G   V   K   D   F   N   E   T   Q   L   A
```

541/170

```
CGG ATT GCG GAC AGT AAG GAT CAT GTG TTT CCC GTG AAT GAC GGC TTT CAG GCT CTG CAA
R   I   A   D   S   K   D   H   V   F   P   V   N   D   G   F   Q   A   L   Q
```

601/190

```
GGC ATC ATC CAC TCA ATT TTG AGC TCT GCT TCC CCA ACC AGC CCT AAG GTC TTC CCT CTC
G   I   I   H   S   I   L   S   S   A   S   P   T   S   P   K   V   F   P   L
```

661/210

```
AGC CTT GAC AGC ACC CCT CAA GAT GGT AAT GTT GTC GTT GCT TGC CTT GTC CAG GGT TTC
S   L   D   S   T   P   Q   D   G   N   V   V   V   A   C   L   V   Q   G   F
```

721/230

```
TTC CCT CAG GAG CCA CTC TCT GTT ACC TGG TCT GAA TCT GGA CAG AAT GTT ACC GCC AGA
F   P   Q   E   P   L   S   V   T   W   S   E   S   G   Q   N   V   T   A   R
```

781/250

```
AAC TTC CCA CCT AGC CAG GAT GCC TCC GGT GAC CTC TAC ACC ACC AGC TCT CAG CTC ACC
```

```
   N    F    P    P    S    Q    D    A    S    G    D    L    Y    T    T    S    S    Q    L    T
841/270

CTT CCA GCC ACC CAG TGC CCA GAT GGT AAG TCC GTT ACC TGC CAT GTT AAG CAC TAC ACC
 L   P   A   T   Q   C   P   D   G   K   S   V   T   C   H   V   K   H   Y   T
901/290

AAC TCC AGC CAG GAT GTT ACT GTT CCA TGC CGT GTT CCA CCA CCT CCA CCA TGC TGC CAC
 N   S   S   Q   D   V   T   V   P   C   R   V   P   P   P   P   P   C   C   H
961/310

CCA CGT CTC TCT CTT CAC CGT CCT GCC CTT GAG GAC TTG CTC TTG GGT TCT GAA GCT AAC
 P   R   L   S   L   H   R   P   A   L   E   D   L   L   L   G   S   E   A   N
1021/330

CTC ACC TGC ACC CTC ACC GGT CTC AGA GAT GCC TCT GGT GCC ACC TTC ACC TGG ACC CCA
 L   T   C   T   L   T   G   L   R   D   A   S   G   A   T   F   T   W   T   P
1081/350

AGC TCT GGT AAG AGC GCT GTT CAA GGA CCA CCT GAG CGT GAC CTC TGT GGA TGC TAC TCT
 S   S   G   K   S   A   V   Q   G   P   P   E   R   D   L   C   G   C   Y   S
1141/370

GTT AGC TCT GTT CTT CCT GGT TGT GCC CAG CCT TGG AAC CAC GGT GAG ACC TTC ACC TGC
 V   S   S   V   L   P   G   C   A   Q   P   W   N   H   G   E   T   F   T   C
1201/390

ACT GCT GCC CAC CCA GAG TTG AAG ACC CCA CTT ACC GCC AAC ATC ACC AAG TCC GGA AAC
 T   A   A   H   P   E   L   K   T   P   L   T   A   N   I   T   K   S   G   N
1261/410

ACC TTC CGT CCC GAG GTC CAC CTC TTG CCA CCA CCA TCT GAG GAG CTT GCC CTC AAT GAG
 T   F   R   P   E   V   H   L   L   P   P   P   S   E   E   L   A   L   N   E
1321/430

CTT GTT ACC CTC ACC TGC CTT GCT CGT GGA TTC AGC CCA AAG GAT GTT CTT GTT AGG TGG
 L   V   T   L   T   C   L   A   R   G   F   S   P   K   D   V   L   V   R   W
1381/450

CTT CAG GGA TCT CAG GAG CTT CCA CGT GAG AAG TAC CTC ACT TGG GCT TCC CGT CAG GAG
 L   Q   G   S   Q   E   L   P   R   E   K   Y   L   T   W   A   S   R   Q   E
1441/470

CCA AGC CAG GGA ACT ACC ACC TAC GCT GTT ACC AGC ATC CTT CGT GTT GCT GCT GAG GAC
 P   S   Q   G   T   T   T   Y   A   V   T   S   I   L   R   V   A   A   E   D
1501/490

TGG AAG AAG GGT GAG ACC TTC TCC TGC ATG GTT GGT CAC GAG GCC CTT CCA CTT GCC TTC
 W   K   K   G   E   T   F   S   C   M   V   G   H   E   A   L   P   L   A   F
1561/510

ACC CAG AAG ACC ATT GAT CGT TTG GCT GGA AAG CCA ACC CAC ATC AAT GTT TCT GTT GTC
 T   Q   K   T   I   D   R   L   A   G   K   P   T   H   I   N   V   S   V   V
1621/530                              1650/538

ATG GCT GAG GCT GAT GGA ACC TGC TAC TAA
```

Figure 2. pGPTV-kan-ocs-ATR-IgA2:

```
                      Bgl II

  1 CTGGCCGGCGCCAGATCTGGGGAACCTGTGGTTGGCATGCACATACAAATGGACGAACGGATAAACCTTTTCACGCCCTT
 81 TTAAATATCCGATTATTCTAATAAACGCTCTTTTCTCTTAGGTTTACCCGCCAATATATCCTGTCAAACACTGATAGTTT
161 AAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAATTAAGGGAGTCACGTTATGACCCCGCCGATGACGCGGG

                                                            EcoR I

241 ACAAGCCGTTTTACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGATCTGAATTCACTGCTTTAAT
321 GAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTCAATTCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGT
401 AGCTCAGATCCTTACCGCCGGTTTCGGTTCATTCTAATGAATATATCACCCGTTACTATCGTATTTTTATGAATAATATT
481 CTCCGTTCAATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAACAATATATTGTGCTGAATAGGT

                                                        Sac I  Asc I

561 TTATAGCGACATCTATGATAGAGCGCCACAATAACAAACAATTGCGTTTTATTATTACAAATCCAATTTTGAGCTCGGCG
641 CGCCAGCTGGACATCATGTTGGATATGAAACAACTATTATTTATCTACATGTTTTAGATGTTATCTGATTATTTTTATAC
721 GTAGTCTTCTATTGATGAGGAGTCTAAGGCTATAGAATTATATATCTAAATGATTAATATATATATTATTAATAATTAAC
801 AATAATTAATATATTATAATTTATATATATATATTTTATATTATTATAATAATATTCTTACAAATATAATTATTATATTC
881 GACGGTATCGGGGCAATTGTATTCGACGGTATCGCGATAAGCTCGCGGATCCCTGAAAGCGACGTTGGATGTTAACATCT
961 ACAAATTGCCTTTTCTTATCGACCATGTACGTAAGCGCTTACGTTTTTGGTGGACCCTTGAGGAAACTGGTAGCTGTTGT
1041 GGGCCTGTGGTCTCAAGATGGATCATTAATTTCCACCTTCACCTACGATGGGGGGCATCGCACCGGTGAGTAATATTGTA
1121 CGGCTAAGAGCGAATTTGGCCTGTAGGATCCCTGAAAGCGACGTTGGATGTTAACATCTACAAATTGCCTTTTCTTATCG
1201 ACCATGTACGTAAGCGCTTACGTTTTTGGTGGACCCTTGAGGAAACTGGTAGCTGTTGTGGGCCTGTGGTCTCAAGATGG
1281 ATCATTAATTTCCACCTTCACCTACGATGGGGGGCATCGCACCGGTGAGTAATATTGTACGGCTAAGAGCGAATTTGGCC
1361 TGTAGGATCCCTGAAAGCGACGTTGGATGTTAACATCTACAAATTGCCTTTTCTTATCGACCATGTACGTAAGCGCTTAC
1441 GTTTTTGGTGGACCCTTGAGGAAACTGGTAGCTGTTGTGGGCCTGTGGTCTCAAGATGGATCATTAATTTCCACCTTCAC
1521 CTACGATGGGGGGCATCGCACCGGTGAGTAATATTGTACGGCTAAGAGCGAATTTGGCCTGTAGGATCCGCGAGCTGGTC
1601 AATCCCATTGCTTTTGAAGCAGCTCAACATTGATCTCTTTCTCGATCGAGGGAGATTTTTCAAATCAGTGCGCAAGACGT
1681 GACGTAAGTATCCGAGTCAGTTTTTATTTTTCTACTAATTTGGTCGTTTATTTCGGCGTGTAGGACATGGCAACCGGGCC
1761 TGAATTTCGCGGGTATTCTGTTTCTATTCCAACTTTTTCTTGATCCGCAGCCATTAACGACTTTTGAATAGATACGCTGA
1841 CACGCCAAGCCTCGCTAGTCAAAAGTGTACCAAACAACGCTTTACAGCAAGAACGGAATGCGCGTGACGCTCGCGGTGAC
1921 GCCATTTCGCCTTTTCAGAAATGGATAAATAGCCTTGCTTCCTATTATATCTTCCCTTAATTAAGGTACCACTTCTCTCA
2001 ATCCAACTTTCTAAACAATGGCTTCTAAACCTTTCTTGTCTCTTCTTTCTTTGTCTTTGCTTTTGTTCACCTCTACTAGT
2081 TTGGCTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAATGAAATCTATTACTTTGTGGAACA
2161 GTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATGTCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAAC
2241 TGACAGAAGACAGAGAACAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATGCAT
2321 GAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGGACAGCCAGCGTCATCATTGCTTT
2401 GACTGATGGAGAACTCCATGAAGATCTCTTTTTCTATTCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTG
2481 TTTACTGTGTTGGTGTGAAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCCGTG
2561 AATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAGCTCTGCTTCCCCAACCAGCCCTAAGGTCTTCCC
2641 TCTCAGCCTTGACAGCACCCCTCAAGATGGTAATGTTGTCGTTGCTTGCCTTGTCCAGGGTTTCTTCCCTCAGGAGCCAC
```

2721 TCTCTGTTACCTGGTCTGAATCTGGACAGAATGTTACCGCCAGAAACTTCCCACCTAGCCAGGATGCCTCCGGTGACCTC

2801 TACACCACCAGCTCTCAGCTCACCCTTCCAGCCACCCAGTGCCCAGATGGTAAGTCCGTTACCTGCCATGTTAAGCACTA

2881 CACCAACTCCAGCCAGGATGTTACTGTTCCATGCCGTGTTCCACCACCTCCACCATGCTGCCACCCACGTCTCTCTCTTC

2961 ACCGTCCTGCCCTTGAGGACTTGCTCTTGGGTTCTGAAGCTAACCTCACCTGCACCCTCACCGGTCTCAGAGATGCCTCT

3041 GGTGCCACCTTCACCTGGACCCCAAGCTCTGGTAAGAGCGCTGTTCAAGGACCACCTGAGCGTGACCTCTGTGGATGCTA

3121 CTCTGTTAGCTCTGTTCTTCCTGGTTGTGCCCAGCCTTGGAACCACGGTGAGACCTTCACCTGCACTGCTGCCCACCCAG

3201 AGTTGAAGACCCCACTTACCGCCAACATCACCAAGTCCGGAAACACCTTCCGTCCCGAGGTCCACCTCTTGCCACCACCA

3281 TCTGAGGAGCTTGCCCTCAATGAGCTTGTTACCCTCACCTGCCTTGCTCGTGGATTCAGCCCAAAGGATGTTCTTGTTAG

3361 GTGGCTTCAGGGATCTCAGGAGCTTCCACGTGAGAAGTACCTCACTTGGGCTTCCCGTCAGGAGCCAAGCCAGGGAACTA

3441 CCACCTACGCTGTTACCAGCATCCTTCGTGTTGCTGCTGAGGACTGGAAGAAGGGTGAGACCTTCTCCTGCATGGTTGGT

3521 CACGAGGCCCTTCCACTTGCCTTCACCCAGAAGACCATTGATCGTTTGGCTGGAAAGCCAACCCACATCAATGTTTCTGT

3601 TGTCATGGCTGAGGCTGATGGAACCTGCTACTAAGATCTGTGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGCTAG

3681 AGCGGCCGCCACCGCGGTGGCGAATTAACAGAGGTGGATGGACAGACCCGTTCTTACACCGGACTGGGCGCGGGATAGGA

3761 TATTCAGATTGGGATGGGATTGAGCTTAAAGCCGGCGCTGAGACCATGCTCAAGGTAGGCAATGTCCTCAGCGTCGAGCC

3841 CGGCATCTATGTCGAGGGCATTGGTGGAGCGCGCTTCGGGGATACCGTGCTTGTAACTGAGACCGGATATGAGGCCCTCA

3921 CTCCGCTTGATCTTGGCAAAGATATTTGACGCATTTATTAGTATGTGTTAATTTTCATTTGCAGTGCAGTATTTTCTATT

4001 CGATCTTTATGTAATTCGTTACAATTAATAAATATTCAAATCAGATTATTGACTGTCATTTGTATCAAATCGTGTTTAAT

4081 GGATATTTTTATTATAATATTGATGATAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTAC

4161 CCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCT<u>GGCGCGCC</u>AAGCTTCACGCTGCCGCAAGCACTCAGGGCG

4241 CAAGGGCTGCTAAAGGAAGCGGAACACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAGCTACT

4321 GGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGGTAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACT

4401 GGGCGGTTTTATGGACAGCAAGCGAACCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTA

4481 AACTGGATGGCTTTCTTGCCGCCAAGGATCTGATGGCGCAGGGGATCAAGATCATGAGCGGAGAATTAAGGGAGTCACGT

4561 TATGACCCCGCCGATGACGCGGGACAAGCCGTTTTACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAG

4641 CCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATACGTCAGAAACCATTATTGCGCGTTCAAAAGTCGCCTAAGGTCAC

4721 TATCAGCTAGCAAATATTTCTTGTCAAAAATGCTCCACTGACGTTCCATAAATTCCCCTCGGTATCCAATTAGAGTCTCA

4801 TATTCACTCTCAATCCAGATCTGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGG

4881 TGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAG

4961 GGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTG

5041 GCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCG

5121 AAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGG

5201 CTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGA

5281 AGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGG

5361 CGCGCATGCCCGACGGCGATGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGC

5441 TTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGC

5521 TGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCT

5601 TCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGAGGATCCCCCGATGAGCTAAGCTAGCTATATCATCAATTT

5681 ATGTATTACACATAATATCGCACTCAGTCTTTCATCTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTC

5761 TGAATTTAAACTTGCATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAATATTT

5841 AAACTATATTTCTTTCAAGATGGGAATTAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTA

5921 CCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCC

6001 CAACAGTTGCGCAGCCTGAATGGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCC

6081 GTCAAGCTCTAAATCGCGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTTG

6161 GGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAG

6241 TGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTGATTTATAAGGGATTTTGCCGATTT

6321 CGGAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGG

6401 CGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCCAGTACATTAAAAACGTCCGCAATGT

6481 GTTATTAAGTTGTCTAAGCGTCAATTTGTTTACACCACAATATATCCTGCCACCAGCCAGCCAACAGCTCCCCGACCGGC

6561 AGCTCGGCACAAAATCACCACTCGATACAGGCAGCCCATCAG

Figure 3. pGPTV-hpt-ocs-35SJ/SC

```
   1 CTGATGGGCTGCCTGTATCGAGTGGTGATTTTGTGCCGAGCTGCCGGTCGGGGAGCTGTTGGCTGGCTGGTGGCAGGATA

  81 TATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACGTTTTTAATGTACTGGGGTGGTTTTTC

 161 TTTTCACCAGTGAGACGGGCAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTG

 241 GTTTGCCCCAGCAGGCGAAAATCCTGTTTGATGGTGGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGCCC

 321 GAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAA

 401 AACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCAC

 481 TAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAG

 561 AAAGCGAAAGGAGCGGGCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCC

 641 AGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACG

 721 ACGGCCAGTGAATTAATTCCCATCTTGAAAGAAATATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAG

 801 TCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTACATT

 881 GCCGTAGATGAAAGACTGAGTGCGATATTATGTGTAATACATAAATTGATGATATAGCTAGCTTAGCTCATCGGGGGATC

 961 CCGGTCGGCATCTACTCTATTCCTTTGCCCTCGGACGAGTGCTGGGGCGTCGGTTTCCACTATCGGCGAGTACTTCTACA

1041 CAGCCATCGGTCCAGACGGCCGCGCTTCTGCGGGCGATTTGTGTACGCCCGACAGTCCCGGCTCCGGATCGGACGATTGC

1121 GTCGCATCGACCCTGCGCCCAAGCTGCATCATCGAAATTGCCGTCAACCAAGCTCTGATAGAGTTGGTCAAGACCAATGC

1201 GGAGCATATACGCCCGGAGCCGCGGCGATCCTGCAAGCTCCGGATGCCTCCGCTCGAAGTAGCGCGTCTGCTGCTCCATA

1281 CAAGCCAACCACGGCCTCCAGAAGAAGATGTTGGCGACCTCGTATTGGGAATCCCCGAACATCGCCTCGCTCCAGTCAAT

1361 GACCGCTGTTATGCGGCCATTGTCCGTCAGGACATTGTTGGAGCCGAAATCCGCGTGCACGAGGTGCCGGACTTCGGGGC

1441 AGTCCTCGGCCCAAAGCATCAGCTCATCGAGAGCCTGCGCGACGGACGCACTGACGGTGTCGTCCATCACAGTTTGCCAG

1521 TGATACACATGGGGATCAGCAATCGCGCATATGAAATCACGCCATGTAGTGTATTGACCGATTCCTTGCGGTCCGAATGG

1601 GCCGAACCCGCTCGTCTGGCTAAGATCGGCCGCAGCGATCGCATCCATGGCCTCCGCGACCGGCTGCAGAACAGCGGGCA

1681 GTTCGGTTTCAGGCAGGTCTTGCAACGTGACACCCTGTGCACGGCGGGAGATGCAATAGGTCAGGCTCTCGCTGAATGCC

1761 CCAATGTCAAGCACTTCCGGAATCGGGAGCGCGGCCGATGCAAAGTGCCGATAAACATAACGATCTTTGTAGAAACCATC

1841 GGCGCAGCTATTTACCCGCAGGACATATCCACGCCCTCCTACATCGAAGCTGAAAGCACGAGATTCTTCGCCCTCCGAGA

1921 GCTGCATCAGGTCGGAGACGCTGTCGAACTTTTCGATCAGAAACTTCTCGACAGACGTCGCGGTGAGTTCAGGCTTTTTC

2001 ATATCTTATTGCCCCCCTAGAGTCGAGATCTGGATTGAGAGTGAATATGAGACTCTAATTGGATACCGAGGGGAATTTAT

2081 GGAACGTCAGTGGAGCATTTTTGACAAGAAATATTTGCTAGCTGATAGTGACCTTAGGCGACTTTTGAACGCGCAATAAT

2161 GGTTTCTGACGTATGTGCTTAGCTCATTAAACTCCAGAAACCCGCGGCTGAGTGGCTCCTTCAACGTTGCGGTTCTGTCA

2241 GTTCCAAACGTAAAACGGCTTGTCCCGCGTCATCGGCGGGGGTCATAACGTGACTCCCTTAATTCTCCGCTCATGATCTT

2321 GATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG

2401 CGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAG

2481 CTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCAGATAGCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTT

2561 TCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTGAAGCTTGG

2641 CGCGCCAGCTGGACATCATGTTGGATATGAAACAACTATTATTTATCTACATGTTTTAGATGTTATCTGATTATTTTTAT

2721 ACGTAGTCTTCTATTGATGAGGAGTCTAAGGCTATAGAATTATATATCTAAATGATTAATATATATATTATTAATAATTA

2801 ACAATAATTAATATATTATAATTTATATATATATATTTTATATTATTATAATAATATTCTTACAAATATAATTATTATAT
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2881  TCGACGGTATCGGGGCAATTGATTCCCGATCCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTA
2961  CAAATGCCATCATTGCGATAAAGGAAAGGCTATCATTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCAC
3041  CCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGAC
3121  GTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGAC
3201  ACGCTGAAATCACCAGTCTCTCTCTACAAGGTACCATGGTGCTCTTCGTGCTCACCTGCCTGCTGGCGGTCTTCCCAGCC
3281  ATCTCCACGAAGAGTCCCATATTTGGTCCCGAGGAGGTGAATAGTGTGGAAGGTAACTCAGTGTCCATCACGTGCTACTA
3361  CCCACCCACCTCTGTCAACCGGCACACCCGGAAGTACTGGTGCCGGCAGGGAGCTAGAGGTGGCTGCATAACCCTCATCT
3441  CCTCGGAGGGCTACGTCTCCAGCAAATATGCAGGCAGGGCTAACCTCACCAACTTCCCGGAGAACGGCACATTTGTGGTG
3521  AACATTGCCCAGCTGAGCCAGGATGACTCCGGGCGCTACAAGTGTGGCCTGGGCATCAATAGCCGAGGCCTGTCCTTTGA
3601  TGTCAGCCTGGAGGTCAGCCAGGGTCCTGGGCTCCTAAATGACACTAAAGTCTACACAGTGGACCTGGGCAGAACGGTGA
3681  CCATCAACTGCCCTTTCAAGACTGAGAATGCTCAAAAGAGGAAGTCCTTGTACAAGCAGATAGGCCTGTACCCTGTGCTG
3761  GTCATCGACTCCAGTGGTTATGTGAATCCCAACTATACAGGAAGAATACGCCTTGATATTCAGGGTACTGGCCAGTTACT
3841  GTTCAGCGTTGTCATCAACCAACTCAGGCTCAGCGATGCTGGGCAGTATCTCTGCCAGGCTGGGGATGATTCCAATAGTA
3921  ATAAGAAGAATGCTGACCTCCAAGTGCTAAAGCCCGAGCCCGAGCTGGTTTATGAAGACCTGAGGGGCTCAGTGACCTTC
4001  CACTGTGCCCTGGGCCCTGAGGTGGCAAACGTGGCCAAATTTCTGTGCCGACAGAGCAGTGGGGAAAACTGTGACGTGGT
4081  CGTCAACACCCTGGGGAAGAGGGCCCCAGCCTTTGAGGGCAGGATCCTGCTCAACCCCCAGGACAAGGATGGCTCATTCA
4161  GTGTGGTGATCACAGGCCTGAGGAAGGAGGATGCAGGGCGCTACCTGTGTGGAGCCCATTCGGATGGTCAGCTGCAGGAA
4241  GGCTCGCCTATCCAGGCCTGGCAACTCTTCGTCAATGAGGAGTCCACGATTCCCCGCAGCCCCACTGTGGTGAAGGGGGT
4321  GGCAGGAAGCTCTGTGGCCGTGCTCTGCCCCTACAACCGTAAGGAAAGCAAAAGCATCAAGTACTGGTGTCTCTGGGAAG
4401  GGGCCCAGAATGGCCGCTGCCCCCTGCTGGTGGACAGCGAGGGGTGGGTTAAGGCCCAGTACGAGGGCCGCCTCTCCCTG
4481  CTGGAGGAGCCAGGCAACGGCACCTTCACTGTCATCCTCAACCAGCTCACCAGCCGGGACGCCGGCTTCTACTGGTGTCT
4561  GACCAACGGCGATACTCTCTGGAGGACCACCGTGGAGATCAAGATTATCGAAGGAGAACCAAACCTCAAGGTTCCCGGGA
4641  ATGTCACGGCTGTGCTGGGAGAGACTCTCAAGGTCCCCTGTCACTTTCCATGCAAATTCTCCTCGTACGAGAAATACTGG
4721  TGCAAGTGGAATAACACGGGCTGCCAGGCCCTGCCCAGCCAAGACGAAGGCCCCAGCAAGGCCTTCGTGAACTGTGACGA
4801  GAACAGCCGGCTTGTCTCCCTGACCCTGAACCTGGTGACCAGGGCTGATGAGGGCTGGTACTGGTGTGGAGTGAAGCAGG
4881  GCCACTTCTATGGAGAGACTGCAGCCGTCTATGTGGCAGTTGAAGAGAGGAAGGCAGCGGGGTCCCGCGATGTCAGCCTA
4961  GCGAAGGCAGACGCTGCTCCTGATGAGAAGGTGCTAGACTCTGGTTTTCGGGAGATTGAGAACAAAGCCATTCAGGATCC
5041  CAGGCTTTTTGCAGAGTGAATTCGTTCGTATCATCGGTTTCGACAACGTTCGTCAAGTTCAATGCATCAGTTTCATTGCG
5121  CACACACCAGAATCCTACTGAGTTCGAGTATTATGGCATTGGGAAAACTGTTTTTCTTGTACCATTTGTTGTGCTTGTAA
5201  TTTACTGTGTTTTTTATTCGGTTTTCGCTATCGAACTGTGAAATGGAAATGGATGGAGAAGAGTTAATGAATGATATGGT
5281  CCTTTTGTTCATTCTCAAATTAATATTATTTGTTTTTTCTCTTATTTGTTGTGTGTTGAATTTGAAATTATAAGAGATAT
5361  GCAAACATTTTGTTTTGAGTAAAAATGTGTCAAATCGTGGCCTCTAATGACCGAAGTTAATATGAGGAGTAAAACACTTG
5441  TAGTTGTCGACGGTATCGATATTAATTCCCGATCCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCAC
5521  CTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCATTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCC
5601  CACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT
5681  GACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAG
5761  GACACGCTGAAATCACCAGTCTCTCTCTAGAGTACCATGGAGAACCATTTGCTTTTCTGGGGAGTCCTGGCGGTTTTTAT
5841  TAAGGCTGTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTTCTTGTTGACAACAAATGTAAGTGTGCCCGGATTACTT
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5921 CCAGGATCATCCGTTCTTCCGAAGATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCCTCTGAACAAC

6001 AGGGAGAATATCTCTGATCCCACCTCACCATTGAGAACCAGATTTGTGTACCATTTGTCTGACCTCTGTAAAAAATGTGA

6081 TCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCTACCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGA

6161 CCTGCTACACTTATGACAGAAACAAGTGCTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGGAA

6241 ACAGCCTTAACCCCAGATGCCTGCTATCCTGACTGAATCCGCGGCGATGAGCTAAGCTAGCTATATCATCAATTTATGTA

6321 TTACACATAATATCGCACTCAGTCTTTCATCTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAAT

6401 TTAAACTTGCATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAATATTTAAACT

6481 ATATTTCTTTCAAGAGCTCAAAATTGGATTTGTAATAATAAAACGCAATTGTTTGTTATTGTGGCGCTCTATCATAGATG

6561 TCGCTATAAACCTATTCAGCACAATATATTGTTTTCATTTTAATATTGTACATATAAGTAGTAGGGTACAATCAGTAAAT

6641 TGAACGGAGAATATTATTCATAAAAATACGATAGTAACGGGTGATATATTCATTAGAATGAACCGAAACCGGCGGTAAGG

6721 ATCTGAGCTACACATGCTCAGGTTTTTTACAACGTGCACAACAGAATTGAAAGCAAATATCATGCGATCATAGGCGTCTC

6801 GCATATCTCATTAAAGCAGTGAATTCAGATCGGCTGAGTGGCTCCTTCAACGTTGCGGTTCTGTCAGTTCCAAACGTAAA

6881 ACGGCTTGTCCCGCGTCATCGGCGGGGTCATAACGTGACTCCCTTAATTCTCCGCTCATGATCAGATTGTCGTTTCCCGC

6961 CTTCAGTTTAAACTATCAGTGTTTGACAGGATATATTGGCGGGTAAACCTAAGAGAAAAGAGCGTTTATTAGAATAATCG

7041 GATATTTAAAAGGGCGTGAAAAGGTTTATCCGTTCGTCCATTTGTATGTGCATGCCAACCACAGGTTCCCCAGATCTGGC

7121 GCCGGCCAG
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